



SEQUENCE LISTING

<110> Werner Seeger

<120> Novel Chimeric Plasminogen Activators and Their Pharmaceutical Use

<130> 607927-000001

<140> US/10/583,785

<141> 2006-06-19

<160> 26

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1143)

<223> Coding sequence of the surfactant protein B precursor

<400> 1

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480

Ser 145	Arg	Gln	Pro	Glu	Pro 150	Glu	Gln	Glu	Pro	Gly 155	Met	Ser	Asp	Pro	Leu 160	
ccc Pro	aaa Lys	cct Pro	ctg Leu	cg Arg 165	gac Asp	cct Pro	ctg Leu	cca Pro	gac Asp 170	cct Pro	ctg Leu	ctg Leu	gac Asp	aag Lys 175	ctc Leu	528
gtc Val	ctc Leu	cct Pro	gtg Val 180	ctg Leu	ccc Pro	ggg Gly	gcc Ala	ctc Leu 185	cag Gln	gcg Ala	agg Arg	cct Pro	ggg Gly 190	cct Pro	cac His	576
aca Thr	cag Gln	gat Asp 195	ctc Leu	tcc Ser	gag Glu	cag Gln	caa Gln 200	ttc Phe	ccc Pro	att Ile	cct Pro	ctc Leu 205	ccc Pro	tat Tyr	tgc Cys	624
tgg Trp	ctc Leu 210	tgc Cys	agg Arg	gct Ala	ctg Leu	atc Ile 215	aag Lys	cg Arg	atc Ile	caa Gln	gcc Ala 220	atg Met	att Ile	ccc Pro	aag Lys	672
ggt Gly 225	gcg Ala	cta Leu	gct Ala	gtg Val	gca Ala 230	gtg Val	gcc Ala	cag Gln	gtg Val	tgc Cys 235	cg Arg	gtg Val	gta Val	cct Pro	ctg Leu 240	720
gtg Val	gcg Ala	ggc Gly	ggc Gly	atc Ile 245	tgc Cys	cag Gln	tgc Cys	ctg Leu	gct Ala 250	gag Glu	cg Arg	tac Tyr	tcc Ser	gtc Val 255	atc Ile	768
ctg Leu	ctc Leu	gac Asp	acg Thr 260	ctg Leu	ctg Leu	ggc Gly	cg Arg	atg Met 265	ctg Leu	ccc Pro	cag Gln	ctg Leu	gtc Val 270	tgc Cys	cg Arg	816
ctc Leu	gtc Val	ctc Leu 275	cg Arg	tgc Cys	tcc Ser	atg Met	gat Asp 280	gac Asp	agc Ser	gct Ala	ggc Gly	cca Pro 285	agg Arg	tcg Ser	ccg Pro	864
aca Thr	gga Gly 290	gaa Glu	tgg Trp	ctg Leu	ccg Pro	cga Arg 295	gac Asp	tct Ser	gag Glu	tgc Cys	cac His 300	ctc Leu	tgc Cys	atg Met	tcc Ser	912
gtg Val 305	acc Thr	acc Thr	cag Gln	gcc Ala	ggg Gly 310	aac Asn	agc Ser	agc Ser	gag Glu	cag Gln 315	gcc Ala	ata Ile	cca Pro	cag Gln	gca Ala 320	960
atg Met	ctc Leu	cag Gln	gcc Ala	tgt Cys 325	gtt Val	ggc Gly	tcc Ser	tgg Trp	ctg Leu 330	gac Asp	agg Arg	gaa Glu	aag Lys	tgc Cys 335	aag Lys	1008
caa Gln	ttt Phe	gtg Val	gag Glu 340	cag Gln	cac His	acg Thr	ccc Pro	cag Gln 345	ctg Leu	ctg Leu	acc Thr	ctg Leu	gtg Val 350	ccc Pro	agg Arg	1056
ggc Gly	tgg Trp	gat Asp 355	gcc Ala	cac His	acc Thr	acc Thr	tgc Cys 360	cag Gln	gcc Ala	ctc Leu	ggg Gly	gtg Val 365	tgt Cys	ggg Gly	acc Thr	1104
atg Met	tcc Ser 370	agc Ser	cct Pro	ctc Leu	cag Gln	tgt Cys 375	atc Ile	cac His	agc Ser	ccc Pro	gac Asp 380	ctt Leu				1143

<210> 2
 <211> 837
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1) ... (837)
 <223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

 <400> 2

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	

aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	
ctc gtc ctc cgg tgc tcc atg	837
Leu Val Leu Arg Cys Ser Met	
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<212> DNA	
<213> Homo sapiens	
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<222> (1) ... (237)	
<223> Coding sequence of the mature surfactant protein B	
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Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys	
1 5 10 15	
cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc	96
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala	
20 25 30	
cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc	144
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys	
35 40 45	
ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc	192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg	
50 55 60	
atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg	237
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met	
65 70 75	
<210> 4	
<211> 1293	

<212> DNA
 <213> Homo sapiens
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 <221> CDS
 <222> (1) ... (1293)
 <223> Coding sequence of the single-chain urokinase-plasminogen activator
 <400> 4

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Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser	
1 5 10 15	
gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac	96
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp	
20 25 30	
tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att	144
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile	
35 40 45	
cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata	192
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile	
50 55 60	
gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga	240
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly	
65 70 75 80	
aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct	288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser	
85 90 95	
gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt	336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu	
100 105 110	
cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg	384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg	
115 120 125	
agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa	432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln	
130 135 140	
gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct	480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro	
145 150 155 160	
cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc	528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg	
165 170 175	
ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg	576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp	
180 185 190	
ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg	624
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val	

195	200	205	
tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His 210 215 220			672
tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly 225 230 235 240			720
cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val 245 250 255			768
gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His 260 265 270			816
cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys 275 280 285			864
gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr 290 295 300			912
aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys 305 310 315 320			960
gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val 325 330 335			1008
gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly 340 345 350			1056
tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys 355 360 365			1104
aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu 370 375 380			1152
caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys 385 390 395 400			1200
gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu 405 410 415			1248
ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu 420 425 430			1293

<210> 5
 <211> 828
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1) ... (828)
 <223> Coding sequence of low mw two-chain urokinase-plasminogen activator

 <400> 5

aag ccc tcc tct cct cca gaa gaa tta aaa ttt cag tgt ggc caa aag	48
Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys	
1 5 10 15	
act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc	96
Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile	
20 25 30	
gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc	144
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly	
35 40 45	
tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg	192
Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val	
50 55 60	
atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac	240
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	
65 70 75 80	
atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag	288
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu	
85 90 95	
atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336
Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	
100 105 110	
gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc	384
Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser	
115 120 125	
aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc	432
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys	
130 135 140	
ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc	480
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile	
145 150 155 160	
act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag	528
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln	
165 170 175	
ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag	576
Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln	
180 185 190	

ccc cac tac tac ggc tct gaa gtc acc acc aaa atg ctg tgt gct gct	624
Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala	
	195
	200
	205
gac cca cag tgg aaa aca gat tcc tgc cag gga gac tca ggg gga ccc	672
Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro	
	210
	215
	220
ctc gtc tgt tcc ctc caa ggc cgc atg act ttg act gga att gtg agc	720
Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser	
	225
	230
	235
	240
tgg ggc cgt gga tgt gcc ctg aag gac aag cca ggc gtc tac acg aga	768
Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg	
	245
	250
	255
gtc tca cac ttc tta ccc tgg atc cgc agt cac acc aag gaa gag aat	816
Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn	
	260
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ggc ctg gcc ctc	828
Gly Leu Ala Leu	
	275

<210> 6
 <211> 1671
 <212> DNA
 <213> Artificial sequence

 <220>
 <221> CDS
 <222> (1) ... (837)
 <223> Coding sequence of human SP-B precursor lacking the C-terminal propeptide

 <220>
 <221> CDS
 <222> (844) ... (1671)
 <223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 6	
atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr	
	1
	5
	10
	15
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
	20
	25
	30
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
	35
	40
	45
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
	50
	55
	60

gcc Ala 65	gat Asp	gac Asp	cta Leu	tgc Cys	caa Gln 70	gag Glu	tgt Cys	gag Glu	gac Asp	atc Ile 75	gtc Val	cac His	atc Ile	ctt Leu	aac Asn 80	240
aag Lys	atg Met	gcc Ala	aag Lys	gag Glu 85	gcc Ala	att Ile	ttc Phe	cag Gln	gac Asp 90	acg Thr	atg Met	agg Arg	aag Lys	ttc Phe 95	ctg Leu	288
gag Glu	cag Gln	gag Glu	tgc Cys 100	aac Asn	gtc Val	ctc Leu	ccc Pro	ttg Leu 105	aag Lys	ctg Leu	ctc Leu	atg Met	ccc Pro 110	cag Gln	tgc Cys	336
aac Asn	caa Gln	gtg Val 115	ctt Leu	gac Asp	gac Asp	tac Tyr	ttc Phe 120	ccc Pro	ctg Leu	gtc Val	atc Ile	gac Asp 125	tac Tyr	ttc Phe	cag Gln	384
aac Asn	cag Gln 130	act Thr	gac Asp	tca Ser	aac Asn	ggc Gly 135	atc Ile	tgt Cys	atg Met	cac His	ctg Leu 140	ggc Gly	ctg Leu	tgc Cys	aaa Lys	432
tcc Ser 145	cgg Arg	cag Gln	cca Pro	gag Glu	cca Pro 150	gag Glu	cag Gln	gag Glu	cca Pro	ggg Gly 155	atg Met	tca Ser	gac Asp	ccc Pro	ctg Leu 160	480
ccc Pro	aaa Lys	cct Pro	ctg Leu	cgg Arg 165	gac Asp	cct Pro	ctg Leu	cca Pro	gac Asp 170	cct Pro	ctg Leu	ctg Leu	gac Asp	aag Lys 175	ctc Leu	528
gtc Val	ctc Leu	cct Pro	gtg Val 180	ctg Leu	ccc Pro	ggg Gly	gcc Ala	ctc Leu 185	cag Gln	gcg Ala	agg Arg	cct Pro	ggg Gly 190	cct Pro	cac His	576
aca Thr	cag Gln	gat Asp 195	ctc Leu	tcc Ser	gag Glu	cag Gln	caa Gln 200	ttc Phe	ccc Pro	att Ile	cct Pro	ctc Leu 205	ccc Pro	tat Tyr	tgc Cys	624
tgg Trp 210	ctc Leu	tgc Cys	agg Arg	gct Ala	ctg Leu	atc Ile 215	aag Lys	cgg Arg	atc Ile	caa Gln	gcc Ala 220	atg Met	att Ile	ccc Pro	aag Lys	672
ggt Gly 225	gcg Ala	cta Leu	gct Ala	gtg Val	gca Ala 230	gtg Val	gcc Ala	cag Gln	gtg Val	tgc Cys 235	cgc Arg	gtg Val	gta Val	cct Pro	ctg Leu 240	720
gtg Val	gcg Ala	ggc Gly	ggc Gly	atc Ile 245	tgc Cys	cag Gln	tgc Cys	ctg Leu	gct Ala 250	gag Glu	cgc Arg	tac Tyr	tcc Ser	gtc Val 255	atc Ile	768
ctg Leu	ctc Leu	gac Asp	acg Thr 260	ctg Leu	ctg Leu	ggc Gly	cgc Arg	atg Met 265	ctg Leu	ccc Pro	cag Gln	ctg Leu	gtc Val 270	tgc Cys	cgc Arg	816
ctc Leu	gtc Val	ctc Leu 275	cgg Arg	tgc Cys	tcc Ser	atg Met	aag Lys 280	ctt Leu	aag Lys	ccc Pro	tcc Ser	tct Ser 285	cct Pro	cca Pro	gaa Glu	864
gaa Glu	tta Leu 290	aaa Lys	ttt Phe	cag Gln	tgt Cys	ggc Gly 295	caa Gln	aag Lys	act Thr	ctg Leu	agg Arg 300	ccc Pro	cgc Arg	ttt Phe	aag Lys	912

att Ile 305	att Ile	ggg Gly	gga Gly	gaa Glu	ttc Phe 310	acc Thr	acc Thr	atc Ile	gag Glu	aac Asn 315	cag Gln	ccc Pro	tgg Trp	ttt Phe	gcg Ala 320	960
gcc Ala	atc Ile	tac Tyr	agg Arg 325	agg Arg	cac His	cgg Arg	ggg Gly	ggc Gly	tct Ser 330	gtc Val	acc Thr	tac Tyr	gtg Val	tgt Cys 335	gga Gly	1008
ggc Gly	agc Ser	ctc Leu	atc Ile 340	agc Ser	cct Pro	tgc Cys	tgg Trp	gtg Val 345	atc Ile	agc Ser	gcc Ala	aca Thr	cac His 350	tgc Cys	ttc Phe	1056
att Ile	gat Asp	tac Tyr 355	cca Pro	aag Lys	aag Lys	gag Glu	gac Asp 360	tac Tyr	atc Ile	gtc Val	tac Tyr	ctg Leu 365	ggg Gly	cgc Arg	tca Ser	1104
agg Arg 370	ctt Leu	aac Asn	tcc Ser	aac Asn	acg Thr	caa Gln 375	ggg Gly	gag Glu	atg Met	aag Lys	ttt Phe 380	gag Glu	gtg Val	gaa Glu	aac Asn	1152
ctc Leu 385	atc Ile	cta Leu	cac His	aag Lys	gac Asp 390	tac Tyr	agc Ser	gct Ala	gac Asp 395	acg Thr 395	ctt Leu	gct Ala	cac His	cac His	aac Asn 400	1200
gac Asp	att Ile	gcc Ala	ttg Leu 405	ctg Leu	aag Lys	atc Ile	cgt Arg	tcc Ser	aag Lys 410	gag Glu	ggc Gly	agg Arg	tgt Cys	gcg Ala 415	cag Gln	1248
cca Pro	tcc Ser	cgg Arg	act Thr 420	ata Ile	cag Gln	acc Thr	atc Ile	tgc Cys 425	ctg Leu	ccc Pro	tgc Ser	atg Met	tat Tyr 430	aac Asn	gat Asp	1296
ccc Pro	cag Gln	ttt Phe 435	ggc Gly	aca Thr	agc Ser	tgt Cys	gag Glu 440	atc Ile	act Thr	ggc Gly	ttt Phe	gga Gly 445	aaa Lys	gag Glu	aat Asn	1344
tct Ser 450	acc Thr	gac Asp	tat Tyr	ctc Leu	tat Tyr	ccg Pro 455	gag Glu	cag Gln	ctg Leu	aaa Lys	atg Met 460	act Thr	ggt Val	gtg Val	aag Lys	1392
ctg Leu 465	att Ile	tcc Ser	cac His	cgg Arg	gag Glu 470	tgt Cys	cag Gln	cag Gln	ccc Pro	cac His 475	tac Tyr	tac Tyr	ggc Gly	tct Ser	gaa Glu 480	1440
gtc Val	acc Thr	acc Thr	aaa Lys	atg Met 485	ctg Leu	tgt Cys	gct Ala	gct Ala	gac Asp 490	cca Pro	cag Gln	tgg Trp	aaa Lys	aca Thr 495	gat Asp	1488
tcc Ser	tgc Cys	cag Gln	gga Gly 500	gac Asp	tca Ser	ggg Gly	gga Gly	ccc Pro 505	ctc Leu	gtc Val	tgt Cys	tcc Ser	ctc Leu 510	caa Gln	ggc Gly	1536
cgc Arg	atg Met	act Thr 515	ttg Leu	act Thr	gga Gly	att Ile	gtg Val 520	agc Ser	tgg Trp	ggc Gly	cgt Arg	gga Gly 525	tgt Cys	gcc Ala	ctg Leu	1584
aag Lys 530	gac Asp	aag Lys	cca Pro	ggc Gly	gtc Val	tac Tyr 535	acg Thr	aga Arg	gtc Val	tca Ser	cac His 540	ttc Phe	tta Leu	ccc Pro	tgg Trp	1632

atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc	1671
Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu	
545 550 555	
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<211> 1674	
<212> DNA	
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<222> (1) ... (837)	
<223> Coding sequence of human SP-B precursor lacking the C-terminal propeptide	
<220>	
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<222> (847) ... (1674)	
<223> Coding sequence of low mw two-chain urokinase-plasminogen activator	
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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480

Ser 145	Arg	Gln	Pro	Glu	Pro 150	Glu	Gln	Glu	Pro	Gly 155	Met	Ser	Asp	Pro	Leu 160	
ccc Pro	aaa Lys	cct Pro	ctg Leu	cgg Arg 165	gac Asp	cct Pro	ctg Leu	cca Pro	gac Asp 170	cct Pro	ctg Leu	ctg Leu	gac Asp	aag Lys 175	ctc Leu	528
gtc Val	ctc Leu	cct Pro	gtg Val 180	ctg Leu	ccc Pro	ggg Gly	gcc Ala	ctc Leu 185	cag Gln	gcg Ala	agg Arg	cct Pro	ggg Gly 190	cct Pro	cac His	576
aca Thr	cag Gln	gat Asp 195	ctc Leu	tcc Ser	gag Glu	cag Gln	caa Gln 200	ttc Phe	ccc Pro	att Ile	cct Pro	ctc Leu 205	ccc Pro	tat Tyr	tgc Cys	624
tgg Trp	ctc Leu 210	tgc Cys	agg Arg	gct Ala	ctg Leu	atc Ile 215	aag Lys	cgg Arg	atc Ile	caa Gln 220	gcc Ala	atg Met	att Ile	ccc Pro	aag Lys	672
ggt Gly 225	gcg Ala	cta Leu	gct Ala	gtg Val 230	gca Ala	gtg Val	gcc Ala	cag Gln	gtg Val	tgc Cys 235	cgc Arg	gtg Val	gta Val	cct Pro	ctg Leu 240	720
gtg Val	gcg Ala	ggc Gly	ggc Gly	atc Ile 245	tgc Cys	cag Gln	tgc Cys	ctg Leu	gct Ala 250	gag Glu	cgc Arg	tac Tyr	tcc Ser	gtc Val 255	atc Ile	768
ctg Leu	ctc Leu	gac Asp	acg Thr 260	ctg Leu	ctg Leu	ggc Gly	cgc Arg	atg Met 265	ctg Leu	ccc Pro	cag Gln	ctg Leu	gtc Val 270	tgc Cys	cgc Arg	816
ctc Leu	gtc Val	ctc Leu 275	cgg Arg	tgc Cys	tcc Ser	atg Met	cag Gln 280	ata Ile	tct Ser	aag Lys	ccc Pro	tcc Ser 285	tct Ser	cct Pro	cca Pro	864
gaa Glu	gaa Glu 290	tta Leu	aaa Lys	ttt Phe	cag Gln	tgt Cys 295	ggc Gly	caa Gln	aag Lys	act Thr	ctg Leu 300	agg Arg	ccc Pro	cgc Arg	ttt Phe	912
aag Lys 305	att Ile	att Ile	ggg Gly	gga Gly	gaa Glu 310	ttc Phe	acc Thr	acc Thr	atc Ile	gag Glu 315	aac Asn	cag Gln	ccc Pro	tgg Trp	ttt Phe 320	960
gcg Ala	gcc Ala	atc Ile	tac Tyr	agg Arg 325	agg Arg	cac His	cgg Arg	ggg Gly	ggc Gly 330	tct Ser	gtc Val	acc Thr	tac Tyr	gtg Val 335	tgt Cys	1008
gga Gly	ggc Gly	agc Ser	ctc Leu 340	atc Ile	agc Ser	cct Pro	tgc Cys	tgg Trp 345	gtg Val	atc Ile	agc Ser	gcc Ala	aca Thr 350	cac His	tgc Cys	1056
ttc Phe	att Ile	gat Asp 355	tac Tyr	cca Pro	aag Lys	aag Lys	gag Glu 360	gac Asp	tac Tyr	atc Ile	gtc Val	tac Tyr 365	ctg Leu	ggg Gly	cgc Arg	1104
tca Ser	agg Arg 370	ctt Leu	aac Asn	tcc Ser	aac Asn	acg Thr 375	caa Gln	ggg Gly	gag Glu	atg Met	aag Lys 380	ttt Phe	gag Glu	gtg Val	gaa Glu	1152
aac	ctc	atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	1200

Asn 385	Leu	Ile	Leu	His	Lys 390	Asp	Tyr	Ser	Ala	Asp 395	Thr	Leu	Ala	His	His 400	
aac Asn	gac Asp	att Ile	gcc Ala	ttg Leu	ctg Leu	aag Lys	atc Ile	cgt Arg	tcc Ser	aag Lys	gag Glu	ggc Gly	agg Arg	tgt Cys	gcg Ala	1248
cag Gln	cca Pro	tcc Ser	cgg Arg	act Thr	ata Ile	cag Gln	acc Thr	atc Ile	tgc Cys	ctg Leu	ccc Pro	tcg Ser	atg Met	tat Tyr	aac Asn	1296
gat Asp	ccc Pro	cag Gln	ttt Phe	ggc Gly	aca Thr	agc Ser	tgt Cys	gag Glu	atc Ile	act Thr	ggc Gly	ttt Phe	gga Gly	aaa Lys	gag Glu	1344
aat Asn	tct Ser	acc Thr	gac Asp	tat Tyr	ctc Leu	tat Tyr	ccg Pro	gag Glu	cag Gln	ctg Leu	aaa Lys	atg Met	act Thr	gtt Val	gtg Val	1392
aag Lys	ctg Leu	att Ile	tcc Ser	cac His	cgg Arg	gag Glu	tgt Cys	cag Gln	cag Gln	ccc Pro	cac His	tac Tyr	tac Tyr	ggc Gly	tct Ser	1440
gaa Glu	gtc Val	acc Thr	acc Thr	aaa Lys	atg Met	ctg Leu	tgt Cys	gct Ala	gct Ala	gac Asp	cca Pro	cag Gln	tgg Trp	aaa Lys	aca Thr	1488
gat Asp	tcc Ser	tgc Cys	cag Gln	gga Gly	gac Asp	tca Ser	ggg Gly	gga Gly	ccc Pro	ctc Leu	gtc Val	tgt Cys	tcc Ser	ctc Leu	caa Gln	1536
ggc Gly	cgc Arg	atg Met	act Thr	ttg Leu	act Thr	gga Gly	att Ile	gtg Val	agc Ser	tgg Trp	ggc Gly	cgt Arg	gga Gly	tgt Cys	gcc Ala	1584
ctg Leu	aag Lys	gac Asp	aag Lys	cca Pro	ggc Gly	gtc Val	tac Tyr	acg Thr	aga Arg	gtc Val	tca Ser	cac His	ttc Phe	tta Leu	ccc Pro	1632
tgg Trp	atc Ile	cgc Arg	agt Ser	cac His	acc Thr	aag Lys	gaa Glu	gag Gln	aat Asn	ggc Gly	ctg Leu	gcc Ala	ctc Leu			1674
<210>	8															
<211>	591															
<212>	DNA															
<213>	Homo sapiens															
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<222>	(1) ... (591)															
<223>	Coding sequence of the surfactant protein C precursor															
<400>	8															
atg Met	gat Asp	gtg Val	ggc Gly	agc Ser	aaa Lys	gag Glu	gtc Val	ctg Leu	atg Met	gag Glu	agc Ser	ccg Pro	ccg Pro	gac Asp	tac Tyr	48
1				5					10					15		

tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
	20 25 30
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val	
	35 40 45
gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac	192
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His	
	50 55 60
acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa	240
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln	
	65 70 75 80
cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc	288
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile	
	85 90 95
ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc	336
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala	
	100 105 110
tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca	384
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro	
	115 120 125
gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc	432
Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe	
	130 135 140
cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag	480
Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys	
	145 150 155 160
ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg	528
Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly	
	165 170 175
gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg	576
Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val	
	180 185 190
ccg ctc tac tac atc	591
Pro Leu Tyr Tyr Ile	
	195

<210> 9
 <211> 174
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1) ... (174)
 <223> Coding sequence of SP-C precursor lacking the C-terminal propeptide

 <400> 9

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val	
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc	174
Val Ile Val Gly Ala Leu Leu Met Gly Leu	
50 55	

<210> 10
 <211> 105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (105)
 <223> Coding sequence of the mature surfactant protein C

<400> 10

ttt ggc att ccc tgc tgc cca gtg cac ctg aaa cgc ctt ctt atc gtg	48
Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val	
1 5 10 15	
gtg gtg gtg gtg gtc ctc atc gtc gtg gtg att gtg gga gcc ctg ctc	96
Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu	
20 25 30	
atg ggt ctc	105
Met Gly Leu	
35	

<210> 11
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (1686)
 <223> Coding sequence of the tissue-plasminogen activator

<400> 11

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5 10 15	
gca gtc ttc gtt tcg ccc agc cag gaa atc cat gcc cga ttc aga aga	96

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	
20 25 30	
gga gcc aga tct tac caa gtg atc tgc aga gat gaa aaa acg cag atg	144
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met	
35 40 45	
ata tac cag caa cat cag tca tgg ctg cgc cct gtg ctc aga agc aac	192
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn	
50 55 60	
cgg gtg gaa tat tgc tgg tgc aac agt ggc agg gca cag tgc cac tca	240
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser	
65 70 75 80	
gtg cct gtc aaa agt tgc agc gag cca agg tgt ttc aac ggg ggc acc	288
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr	
85 90 95	
tgc cag cag gcc ctg tac ttc tca gat ttc gtg tgc cag tgc ccc gaa	336
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu	
100 105 110	
gga ttt gct ggg aag tgc tgt gaa ata gat acc agg gcc acg tgc tac	384
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr	
115 120 125	
gag gac cag ggc atc agc tac agg ggc acg tgg agc aca gcg gag agt	432
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser	
130 135 140	
ggc gcc gag tgc acc aac tgg aac agc agc gcg ttg gcc cag aag ccc	480
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro	
145 150 155 160	
tac agc ggg cgg agg cca gat gcc atc agg ctg ggc ctg ggg aac cac	528
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His	
165 170 175	
aac tac tgc aga aac cca gat cga gac tca aag ccc tgg tgc tac gtc	576
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val	
180 185 190	
ttt aag gcg ggg aag tac agc tca gag ttc tgc agc acc cct gcc tgc	624
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys	
195 200 205	
tct gag gga aac agt gac tgc tac ttt ggg aat ggg tca gcc tac cgt	672
Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg	
210 215 220	
ggc acg cac agc ctc acc gag tgc ggt gcc tcc tgc ctc ccg tgg aat	720
Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn	
225 230 235 240	
tcc atg atc ctg ata ggc aag gtt tac aca gca cag aac ccc agt gcc	768
Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala	
245 250 255	
cag gca ctg ggc ctg ggc aaa cat aat tac tgc cgg aat cct gat ggg	816

Gln	Ala	Leu	Gly 260	Leu	Gly	Lys	His	Asn 265	Tyr	Cys	Arg	Asn	Pro 270	Asp	Gly	
gat Asp	gcc Ala	aag Lys 275	ccc Pro	tgg Trp	tgc Cys	cac His	gtg Val 280	ctg Leu	aag Lys	aac Asn	cgc Arg	agg Arg 285	ctg Leu	acg Thr	tgg Trp	864
gag Glu	tac Tyr 290	tgt Cys	gat Asp	gtg Val	ccc Pro	tcc Ser 295	tgc Cys	tcc Ser	acc Thr	tgc Cys	ggc Gly 300	ctg Leu	aga Arg	cag Gln	tac Tyr	912
agc Ser 305	cag Gln	cct Pro	cag Gln	ttt Phe	cgc Arg 310	atc Ile	aaa Lys	gga Gly	ggg Gly	ctc Leu 315	ttc Phe	gcc Ala	gac Asp	atc Ile	gcc Ala 320	960
tcc Ser	cac His	ccc Pro	tgg Trp	cag Gln 325	gct Ala	gcc Ala	atc Ile	ttt Phe	gcc Ala 330	aag Lys	cac His	agg Arg	agg Arg	tcg Ser 335	ccc Pro	1008
gga Gly	gag Glu	cgg Arg	ttc Phe 340	ctg Leu	tgc Cys	ggg Gly	ggc Gly	ata Ile 345	ctc Leu	atc Ile	agc Ser	tcc Ser	tgc Cys 350	tgg Trp	att Ile	1056
ctc Leu	tct Ser	gcc Ala 355	gcc Ala	cac His	tgc Cys	ttc Phe	cag Gln 360	gag Glu	agg Arg	ttt Phe	ccg Pro	ccc Pro 365	cac His	cac His	ctg Leu	1104
acg Thr	gtg Val 370	atc Ile	ttg Leu	ggc Gly	aga Arg	aca Thr 375	tac Tyr	cgg Arg	gtg Val	gtc Val	cct Pro 380	ggc Gly	gag Glu	gag Glu	gag Glu	1152
cag Gln 385	aaa Lys	ttt Phe	gaa Glu	gtc Val	gaa Glu 390	aaa Lys	tac Tyr	att Ile	gtc Val	cat His 395	aag Lys	gaa Glu	ttc Phe	gat Asp	gat Asp 400	1200
gac Asp	act Thr	tac Tyr	gac Asp	aat Asn 405	gac Asp	att Ile	gcg Ala	ctg Leu	ctg Leu 410	cag Gln	ctg Leu	aaa Lys	tcg Ser	gat Asp 415	tcg Ser	1248
tcc Ser	cgc Arg	tgt Cys	gcc Ala 420	cag Gln	gag Glu	agc Ser	agc Ser	gtg Val 425	gtc Val	cgc Arg	act Thr	gtg Val	tgc Cys 430	ctt Leu	ccc Pro	1296
ccg Pro	gcg Ala	gac Asp 435	ctg Leu	cag Gln	ctg Leu	ccg Pro	gac Asp 440	tgg Trp	acg Thr	gag Glu	tgt Cys	gag Glu 445	ctc Leu	tcc Ser	ggc Gly	1344
tac Tyr	ggc Gly 450	aag Lys	cat His	gag Glu	gcc Ala	ttg Leu 455	tct Ser	cct Pro	ttc Phe	tat Tyr	tcg Ser 460	gag Glu	cgg Arg	ctg Leu	aag Lys	1392
gag Glu 465	gct Ala	cat His	gtc Val	aga Arg	ctg Leu 470	tac Tyr	cca Pro	tcc Ser	agc Ser	cgc Arg 475	tgc Cys	aca Thr	tca Ser	caa Gln	cat His 480	1440
tta Leu	ctt Leu	aac Asn	aga Arg	aca Thr 485	gtc Val	acc Thr	gac Asp	aac Asn	atg Met 490	ctg Leu	tgt Cys	gct Ala	gga Gly	gac Asp 495	act Thr	1488
cgg	agc	ggc	ggg	ccc	cag	gca	aac	ttg	cac	gac	gcc	tgc	cag	ggc	gat	1536

Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp	
500 505 510	
tcg gga ggc ccc ctg gtg tgt ctg aac gat ggc cgc atg act ttg gtg	1584
Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val	
515 520 525	
ggc atc atc agc tgg ggc ctg ggc tgt gga cag aag gat gtc ccg ggt	1632
Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly	
530 535 540	
gtg tac acc aag gtt acc aac tac cta gac tgg att cgt gac aac atg	1680
Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met	
545 550 555 560	
cga ccg	1686
Arg Pro	

<210> 12
 <211> 1158
 <212> DNA
 <213> Artificial sequence

<220>
 <221> sig_peptide
 <222> (1) ... (69)
 <223> Signal sequence of the human surfactant protein B

<220>
 <221> CDS
 <222> (76) ... (312)
 <223> Coding sequence of the mature human surfactant protein B

<220>
 <221> CDS
 <222> (313) ... (1140)
 <223> Coding sequence of human low mw two-chain urokinase-plasminogen activator

<220>
 <221> CDS
 <222> (1141) ... (1158)
 <223> Hexahistidine affinity tag

<400> 12

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg ttc ccc att cct ctc ccc tat	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr	
20 25 30	
tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc	144
Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro	
35 40 45	
aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct	192

Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	
	50					55					60					
ctg	gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	ctg	gct	gag	cgc	tac	tcc	gtc	240
Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	
	65				70					75					80	
atc	ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	atg	ctg	ccc	cag	ctg	gtc	tgc	288
Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	
				85					90					95		
cgc	ctc	gtc	ctc	cgg	tgc	tcc	atg	aag	ccc	tcc	tct	cct	cca	gaa	gaa	336
Arg	Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	
				100				105					110			
tta	aaa	ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	aag	att	384
Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	
		115					120					125				
att	ggg	gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	gcg	gcc	432
Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	
	130					135					140					
atc	tac	agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	gga	ggc	480
Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	
	145				150					155					160	
agc	ctc	atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	ttc	att	528
Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	
				165					170					175		
gat	tac	cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggt	cgc	tca	agg	576
Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	
			180					185					190			
ctt	aac	tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	aac	ctc	624
Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	
		195				200						205				
atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	aac	gac	672
Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	
	210					215					220					
att	gcc	ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	cag	cca	720
Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	
	225				230					235					240	
tcc	cgg	act	ata	cag	acc	atc	tgc	ctg	ccc	tcg	atg	tat	aac	gat	ccc	768
Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	
				245					250					255		
cag	ttt	ggc	aca	agc	tgt	gag	atc	act	ggc	ttt	gga	aaa	gag	aat	tct	816
Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	
			260					265					270			
acc	gac	tat	ctc	tat	ccg	gag	cag	ctg	aaa	atg	act	gtt	gtg	aag	ctg	864
Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu	
		275					280					285				
att	tcc	cac	cgg	gag	tgt	cag	cag	ccc	cac	tac	tac	ggc	tct	gaa	gtc	912

Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val		
	290					295					300						
acc	acc	aaa	atg	ctg	tgt	gct	gct	gac	cca	cag	tgg	aaa	aca	gat	tcc		960
Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser		
	305				310					315					320		
tgc	cag	gga	gac	tca	ggg	gga	ccc	ctc	gtc	tgt	tcc	ctc	caa	ggc	cgc		1008
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg		
				325					330					335			
atg	act	ttg	act	gga	att	gtg	agc	tgg	ggc	cgt	gga	tgt	gcc	ctg	aag		1056
Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys		
			340					345					350				
gac	aag	cca	ggc	gtc	tac	acg	aga	gtc	tca	cac	ttc	tta	ccc	tgg	atc		1104
Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	Pro	Trp	Ile		
		355					360					365					
cgc	agt	cac	acc	aag	gaa	gag	aat	ggc	ctg	gcc	ctc	cat	cat	cat	cat		1152
Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	His	His	His	His		
	370					375					380						
cat	cat																1158
His	His																
	385																

<210> 13
 <211> 1149
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> sig_peptide
 <222> (1) ... (60)
 <223> Signal sequence of the human urokinase plasminogen activator

<220>
 <221> CDS
 <222> (67) ... (894)
 <223> Coding sequence of human low mw two-chain urokinase-plasminogen activator

<220>
 <221> CDS
 <222> (895) ... (1131)
 <223> Coding sequence of the mature human surfactant protein B

<220>
 <221> CDS
 <222> (1132) ... (1149)
 <223> Hexahistidine affinity tag

<400> 13

atg	aga	gcc	ctg	ctg	gcg	cgc	ctg	ctt	ctc	tgc	gtc	ctg	gtc	gtg	agc		48
Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser		
	1			5					10					15			

gac Asp	tcc Ser	aaa Lys	ggc Gly 20	agc Ser	aat Asn	aag Lys	ccc Pro	tcc Ser 25	tct Ser	cct Pro	cca Pro	gaa Glu	gaa Glu 30	tta Leu	aaa Lys	96
ttt Phe	cag Gln	tgt Cys 35	ggc Gly	caa Gln	aag Lys	act Thr	ctg Leu 40	agg Arg	ccc Pro	cgc Arg	ttt Phe	aag Lys 45	att Ile	att Ile	ggg Gly	144
gga Gly	gaa Glu 50	ttc Phe	acc Thr	acc Thr	atc Ile	gag Glu 55	aac Asn	cag Gln	ccc Pro	tgg Trp	ttt Phe 60	gcg Ala	gcc Ala	atc Ile	tac Tyr	192
agg Arg 65	agg Arg	cac His	cgg Arg	ggg Gly	ggc Gly 70	tct Ser	gtc Val	acc Thr	tac Tyr	gtg Val 75	tgt Cys	gga Gly	ggc Gly	agc Ser	ctc Leu 80	240
atc Ile	agc Ser	cct Pro	tgc Cys	tgg Trp 85	gtg Val	atc Ile	agc Ser	gcc Ala	aca Thr 90	cac His	tgc Cys	ttc Phe	att Ile	gat Asp 95	tac Tyr	288
cca Pro	aag Lys	aag Lys	gag Glu 100	gac Asp	tac Tyr	atc Ile	gtc Val	tac Tyr 105	ctg Leu	ggt Gly	cgc Arg	tca Ser	agg Arg 110	ctt Leu	aac Asn	336
tcc Ser	aac Asn	acg Thr 115	caa Gln	ggg Gly	gag Glu	atg Met	aag Lys 120	ttt Phe	gag Glu	gtg Val	gaa Glu	aac Asn 125	ctc Leu	atc Ile	cta Leu	384
cac His 130	aag Lys	gac Asp	tac Tyr	agc Ser	gct Ala	gac Asp 135	acg Thr	ctt Leu	gct Ala	cac His	cac His 140	aac Asn	gac Asp	att Ile	gcc Ala	432
ttg Leu 145	ctg Leu	aag Lys	atc Ile	cgt Arg	tcc Ser 150	aag Lys	gag Glu	ggc Gly	agg Arg	tgt Cys 155	gcg Ala	cag Gln	cca Pro	tcc Ser	cgg Arg 160	480
act Thr	ata Ile	cag Gln	acc Thr	atc Ile 165	tgc Cys	ctg Leu	ccc Pro	tcg Ser	atg Met 170	tat Tyr	aac Asn	gat Asp	ccc Pro	cag Gln 175	ttt Phe	528
ggc Gly	aca Thr	agc Ser	tgt Cys 180	gag Glu	atc Ile	act Thr	ggc Gly 185	ttt Phe	gga Gly	aaa Lys	gag Glu	aat Asn	tct Ser 190	acc Thr	gac Asp	576
tat Tyr	ctc Leu	tat Tyr 195	ccg Pro	gag Glu	cag Gln	ctg Leu	aaa Lys 200	atg Met	act Thr	gtt Val	gtg Val	aag Lys 205	ctg Leu	att Ile	tcc Ser	624
cac His 210	cgg Arg	gag Glu	tgt Cys	cag Gln	cag Gln	ccc Pro 215	cac His	tac Tyr	tac Tyr	ggc Gly	tct Ser 220	gaa Glu	gtc Val	acc Thr	acc Thr	672
aaa Lys 225	atg Met	ctg Leu	tgt Cys	gct Ala	gct Ala 230	gac Asp	cca Pro	cag Gln	tgg Trp	aaa Lys 235	aca Thr	gat Asp	tcc Ser	tgc Cys	cag Gln 240	720
gga Gly	gac Asp	tca Ser	ggg Gly	gga Gly 245	ccc Pro	ctc Leu	gtc Val	tgt Cys	tcc Ser 250	ctc Leu	caa Gln	ggc Gly	cgc Arg	atg Met 255	act Thr	768

ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag gac aag	816
Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys	
	260
cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc cgc agt	864
Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser	
	275
cac acc aag gaa gag aat ggc ctg gcc ctc ttc ccc att cct ctc ccc	912
His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro	
	290
tat tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att	960
Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile	
	305
ccc aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta	1008
Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val	
	325
cct ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc	1056
Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser	
	340
gtc atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc	1104
Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val	
	355
tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat cat	1149
Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His	
	370

<210> 14
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>

<221> PEPTIDE
 <222> (1) ... (381)
 <223> Surfactant protein B precursor

<400> 14

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr	
1 5 10 15	
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	

Lys Met Ala Lys Glu₈₅ Ala Ile Phe Gln Asp₉₀ Thr Met Arg Lys Phe₉₅ Leu
 Glu Gln Glu Cys₁₀₀ Asn Val Leu Pro Leu₁₀₅ Lys Leu Leu Met Pro₁₁₀ Gln Cys
 Asn Gln Val₁₁₅ Leu Asp Asp Tyr Phe₁₂₀ Pro Leu Val Ile Asp₁₂₅ Tyr Phe Gln
 Asn Gln₁₃₀ Thr Asp Ser Asn Gly₁₃₅ Ile Cys Met His Leu₁₄₀ Gly Leu Cys Lys
 Ser₁₄₅ Arg Gln Pro Glu Pro₁₅₀ Glu Gln Glu Pro Gly₁₅₅ Met Ser Asp Pro Leu₁₆₀
 Pro Lys Pro Leu Arg₁₆₅ Asp Pro Leu Pro Asp₁₇₀ Pro Leu Leu Asp Lys₁₇₅ Leu
 Val Leu Pro Val₁₈₀ Leu Pro Gly Ala Leu₁₈₅ Gln Ala Arg Pro Gly₁₉₀ Pro His
 Thr Gln Asp₁₉₅ Leu Ser Glu Gln Gln₂₀₀ Phe Pro Ile Pro Leu₂₀₅ Pro Tyr Cys
 Trp Leu₂₁₀ Cys Arg Ala Leu Ile₂₁₅ Lys Arg Ile Gln Ala₂₂₀ Met Ile Pro Lys
 Gly₂₂₅ Ala Leu Ala Val Ala₂₃₀ Val Ala Gln Val Cys₂₃₅ Arg Val Val Pro Leu₂₄₀
 Val Ala Gly Gly Ile₂₄₅ Cys Gln Cys Leu Ala₂₅₀ Glu Arg Tyr Ser Val₂₅₅ Ile
 Leu Leu Asp Thr₂₆₀ Leu Leu Gly Arg Met₂₆₅ Leu Pro Gln Leu Val₂₇₀ Cys Arg
 Leu Val Leu₂₇₅ Arg Cys Ser Met Asp₂₈₀ Asp Ser Ala Gly Pro₂₈₅ Arg Ser Pro
 Thr Gly₂₉₀ Glu Trp Leu Pro Arg₂₉₅ Asp Ser Glu Cys His₃₀₀ Leu Cys Met Ser
 Val₃₀₅ Thr Thr Gln Ala Gly₃₁₀ Asn Ser Ser Glu Gln₃₁₅ Ala Ile Pro Gln Ala₃₂₀
 Met Leu Gln Ala Cys₃₂₅ Val Gly Ser Trp Leu₃₃₀ Asp Arg Glu Lys Cys₃₃₅ Lys
 Gln Phe Val Glu₃₄₀ Gln His Thr Pro Gln₃₄₅ Leu Leu Thr Leu Val₃₅₀ Pro Arg
 Gly Trp Asp₃₅₅ Ala His Thr Thr Cys₃₆₀ Gln Ala Leu Gly Val₃₆₅ Cys Gly Thr
 Met Ser₃₇₀ Ser Pro Leu Gln Cys₃₇₅ Ile His Ser Pro Asp₃₈₀ Leu

<210> 15

<211> 279
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> PEPTIDE
 <222> (1) ... (279)
 <223> Surfactant protein B precursor lacking the C-terminal propeptide
 <400> 15

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
 1 5 10 15
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
 20 25 30
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
 35 40 45
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
 50 55 60
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
 65 70 75 80
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
 85 90 95
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
 100 105 110
 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
 115 120 125
 Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
 130 135 140
 Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
 145 150 155 160
 Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
 165 170 175
 Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
 180 185 190
 Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
 195 200 205
 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
 210 215 220
 Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
 225 230 235 240
 Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
 245 250 255
 Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg

260 265 270

Leu Val Leu Arg Cys Ser Met
275

<210> 16
<211> 79
<212> PRT
<213> Homo sapiens
<220>
<221> PEPTIDE
<222> (1) ... (79)
<223> Mature surfactant protein B
<400> 16

Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys
1 5 10 15
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
20 25 30
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
35 40 45
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
50 55 60
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
65 70 75

<210> 17
<211> 431
<212> PRT
<213> Homo sapiens
<220>
<221> PEPTIDE
<222> (1) ... (431)
<223> Single-chain urokinase-plasminogen activator
<400> 17

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1 5 10 15
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
20 25 30
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35 40 45
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50 55 60
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly

65					70					75				80
Lys	Ala	Ser	Thr	Asp	Thr	Met	Gly	Arg	Pro	Cys	Leu	Pro	Trp	Ser
				85					90				Asn	95
Ala	Thr	Val	Leu	Gln	Gln	Thr	Tyr	His	Ala	His	Arg	Ser	Asp	Ala
			100					105					110	Leu
Gln	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asn
		115					120					125		Arg
Arg	Arg	Pro	Trp	Cys	Tyr	Val	Gln	Val	Gly	Leu	Lys	Pro	Leu	Val
	130					135					140			Gln
Glu	Cys	Met	Val	His	Asp	Cys	Ala	Asp	Gly	Lys	Lys	Pro	Ser	Ser
145					150					155				Pro
Pro	Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro
				165					170					Arg
Phe	Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro
			180					185					190	Trp
Phe	Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr
		195					200					205		Val
Cys	Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr
	210					215					220			His
Cys	Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu
225					230					235				Gly
Arg	Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu
				245					250					Val
Glu	Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala
			260					265					270	His
His	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg
		275					280					285		Cys
Ala	Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met
	290					295					300			Tyr
Asn	Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly
305					310					315				Lys
Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr
				325					330					Val
Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr
			340					345				350		Gly
Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp
		355					360					365		Lys
Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser
	370					375					380			Leu
Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly
														Cys

Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 210 215 220
 Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser
 225 230 235 240
 Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg
 245 250 255
 Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn
 260 265 270
 Gly Leu Ala Leu
 275

<210> 19
 <211> 557
 <212> PRT
 <213> Artificial sequence

<220>
 <221> PEPTIDE
 <222> (1) ... (279)
 <223> Human surfactant protein B precursor lacking the C-terminal propeptide

<220>
 <221> PEPTIDE
 <222> (282) ... (577)
 <223> Human low molecular weight two-chain urokinase-plasminogen activator
 <400> 19

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
 1 5 10 15
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
 20 25 30
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
 35 40 45
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
 50 55 60
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
 65 70 75 80
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
 85 90 95
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
 100 105 110
 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
 115 120 125
 Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
 130 135 140

Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
 145 150 155 160
 Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
 165 170 175
 Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
 180 185 190
 Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
 195 200 205
 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
 210 215 220
 Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
 225 230 235 240
 Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
 245 250 255
 Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
 260 265 270
 Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu
 275 280 285
 Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys
 290 295 300
 Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala
 305 310 315 320
 Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly
 325 330 335
 Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe
 340 345 350
 Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser
 355 360 365
 Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn
 370 375 380
 Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn
 385 390 395 400
 Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln
 405 410 415
 Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp
 420 425 430
 Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn
 435 440 445
 Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys
 450 455 460

Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu
 465 470 475 480
 Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp
 485 490 495
 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly
 500 505 510
 Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu
 515 520 525
 Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp
 530 535 540
 Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu
 545 550 555

<210> 20
 <211> 558
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> PEPTIDE
 <222> (1) ... (279)
 <223> Human surfactant protein B precursor lacking the C-terminal propeptide

<220>
 <221> PEPTIDE
 <222> (283) ... (558)
 <223> Human low molecular weight two-chain urokinase-plasminogen activator

<400> 20

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr
 1 5 10 15
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
 20 25 30
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
 35 40 45
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
 50 55 60
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
 65 70 75 80
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
 85 90 95
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
 100 105 110
 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln

115					120					125					
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys
	130					135					140				
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu
145					150					155					160
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu
				165					170					175	
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His
			180					185					190		
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys
		195					200					205			
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys
	210					215					220				
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu
225					230					235					240
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile
				245					250					255	
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg
			260					265					270		
Leu	Val	Leu	Arg	Cys	Ser	Met	Gln	Ile	Ser	Lys	Pro	Ser	Ser	Pro	Pro
		275					280					285			
Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe
	290					295					300				
Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe
305					310					315					320
Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys
				325					330					335	
Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys
			340					345					350		
Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg
		355					360					365			
Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu
	370					375					380				
Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His
385					390					395					400
Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala
				405					410					415	
Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn
			420					425					430		
Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu

435	440	445
Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val		
450	455	460
Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser		
465	470	475
Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr		
485	490	495
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln		
500	505	510
Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala		
515	520	525
Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro		
530	535	540
Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu		
545	550	555

<210> 21
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (197)
 <223> Surfactant protein C precursor

<400> 21

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr		
1	5	10
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His		
20	25	30
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val		
35	40	45
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His		
50	55	60
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln		
65	70	75
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile		
85	90	95
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala		
100	105	110
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro		
115	120	125

Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe
 130 135 140
 Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys
 145 150 155 160
 Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly
 165 170 175
 Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val
 180 185 190
 Pro Leu Tyr Tyr Ile
 195

<210> 22
 <211> 58
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (58)
 <223> Surfactant protein C precursor lacking the C-terminal
 propeptide

<400> 22

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
 1 5 10 15
 Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
 20 25 30
 Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val
 35 40 45
 Val Ile Val Gly Ala Leu Leu Met Gly Leu
 50 55

<210> 23
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (35)
 <223> Mature surfactant protein C

<400> 23

Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val
 1 5 10 15
 Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu
 20 25 30

Met Gly Leu
35

<210> 24
<211> 562
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (562)
<223> Tissue-plasminogen activator

<400> 24

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
20 25 30
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
35 40 45
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
50 55 60
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65 70 75 80
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
85 90 95
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
100 105 110
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
115 120 125
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
130 135 140
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
145 150 155 160
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
165 170 175
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
180 185 190
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
195 200 205
Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
210 215 220
Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
225 230 235 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
 245 250 255
 Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
 260 265 270
 Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
 275 280 285
 Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr
 290 295 300
 Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala
 305 310 315 320
 Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro
 325 330 335
 Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile
 340 345 350
 Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu
 355 360 365
 Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu
 370 375 380
 Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp
 385 390 395 400
 Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
 405 410 415
 Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
 420 425 430
 Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
 435 440 445
 Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
 450 455 460
 Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
 465 470 475 480
 Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
 485 490 495
 Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
 500 505 510
 Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
 515 520 525
 Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
 530 535 540
 Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
 545 550 555 560

Arg Pro

<210> 25
 <211> 386
 <212> PRT
 <213> Artificial sequence

<220>
 <221> SIGNAL
 <222> (1) ... (23)
 <223> Signal sequence of the human surfactant protein B

<220>
 <221> PEPTIDE
 <222> (26) ... (104)
 <223> Mature human surfactant protein B

<220>
 <221> PEPTIDE
 <222> (105) ... (380)
 <223> Human low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> PEPTIDE
 <222> (381) ... (386)
 <223> Hexahistidine affinity tag

<400> 25

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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr
 1          5          10          15
Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr
          20          25          30
Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro
          35          40          45
Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro
 50          55          60
Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val
 65          70          75          80
Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys
          85          90          95
Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu
          100          105          110
Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile
          115          120          125
Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala
          130          135          140
Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly

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145 150 155 160
 Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile
 165 170 175
 Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg
 180 185 190
 Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu
 195 200 205
 Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp
 210 215 220
 Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro
 225 230 235 240
 Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro
 245 250 255
 Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser
 260 265 270
 Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu
 275 280 285
 Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val
 290 295 300
 Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser
 305 310 315 320
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg
 325 330 335
 Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys
 340 345 350
 Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile
 355 360 365
 Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His
 370 375 380
 His His
 385

<210> 26
 <211> 383
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> SIGNAL
 <222> (1) ... (20)
 <223> Signal sequence of the human urokinase plasminogen activator

 <220>
 <221> PEPTIDE

<222> (23) ... (298)
 <223> Human low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> PEPTIDE
 <222> (299) ... (377)
 <223> Coding sequence of the mature human surfactant protein B

<220>
 <221> PEPTIDE
 <222> (378) ... (383)
 <223> Hexahistidine affinity tag

<400> 26

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Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
 1          5          10
Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys
          20          25          30
Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly
          35          40          45
Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr
 50          55          60
Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu
 65          70          75          80
Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp Tyr
          85          90          95
Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn
          100          105          110
Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu
          115          120          125
His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala
          130          135          140
Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg
          145          150          155          160
Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe
          165          170          175
Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp
          180          185          190
Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser
          195          200          205
His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr
          210          215          220
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln

```

225		230		235		240
Gly Asp Ser Gly Gly	Pro Leu Val Cys	Ser Leu Gln Gly Arg	Met Thr			
	245	250	255			
Leu Thr Gly Ile Val Ser Trp Gly Arg	Gly Cys Ala Leu Lys Asp Lys					
	260	265	270			
Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser						
	275	280	285			
His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro						
	290	295	300			
Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile						
	305	310	315			320
Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val						
	325	330	335			
Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser						
	340	345	350			
Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val						
	355	360	365			
Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His						
	370	375	380			